Table S3: Primers sets used in qPCR of *merA* and *gyrA* in strains AAS1 and R1-1.[1]

Name[2]	Start Position[3]	Tm (°C)	Sequence (5' to 3')	Amplicon Length
HBgyrA-F	441	58	TGTCATGGAGCCTCAGGTTCT	66
HBgyrA-R	506	57	ATGCCTGTAGTACCGTTGCAAA	
HBmerA-F	441	59	ATGCGGCAGGAGATTGTGTT	71
HBmerA-R	506	58	GCTGCTATCCCTCCTTCCATAG	
HVgyrA-F	14	57	ACAGGTATTGCTGTTGGACTTTCA	107
HVgyrA-R	120	55	TCCTCAACAGTTGCATTTGGAA	
HVmerA-F	1049	59	AGAGCCTCGGGCTTGATAGG	70
HVmerA-R	1118	59	AGAAACTCGTTCACCTTCACGAA	

[1]PCR reactions for all primers included consisted of an initial denaturation stage of 90° C for 10 minutes, then 45 cycles of 90° C for 15 seconds followed by 1 minute at 55° C. Upon completion, a melt curve was performed to verify identity of the amplification products.

[2]All primer sets shown were designed for this study.

[3]Nucleotide numbering for each primer set is according to the relative nucleotide position within the *merA* or *gyrA* locus in the genomes of AAS1 and R1-1. Target accession numbers are given in Materials and Methods.